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RAW SEQUENCE LISTING   DATE: 12/18/2002
PATENT APPLICATION: US/09/783,338B   TIME: 12:10:21

Input Set : **A:\ziegler.ST25.txt**
Output Set: **N:\CRF4\12182002\I783338B.raw**

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  4 <110> APPLICANT: Ziegler, Petra
  6        Eggeling, Lothar
  8        Sahm, Hermann
 10        Thierbach, Georg
 13 <120> TITLE OF INVENTION: NEW NUCLEOTIDE SEQUENCES CODING FOR THE THRE GENE AND
 14        PROCESS FOR
 15        ENZYMATIC PRODUCTION OF L-THREONINE USING CORYNEFORM BACTERIA
 18 <130> FILE REFERENCE: 21123/277066
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C--> 20 **<140> CURRENT APPLICATION NUMBER: US/09/783,338B**
C--> 20 **<141> CURRENT FILING DATE: 2001-02-14**
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 20 <160> NUMBER OF SEQ ID NOS: 8
 22 <170> SOFTWARE: PatentIn version 3.0
 26 <210> SEQ ID NO: 1
 28 <211> LENGTH: 2817
 30 <212> TYPE: DNA
 32 <213> ORGANISM: Corynebacterium glutamicum ATCC14752
 34 <220> FEATURE:
 36 <221> NAME/KEY: CDS
 38 <222> LOCATION: (398)..(1864)
 41 <400> SEQUENCE: 1
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 46 tcaagccaaa aaggggcatt ttcattaaga aaatacccct ttgacctggt gttattgagc     180
 48 tggagaagag acttgaactc tcaacctacg cattacaagt gcgttgcgct gccaattgcg     240
 50 ccactccagc accgcagatg ctgatgatca acaactacga atacgtatct tagcgtatgt     300
 52 gtacatcaca atggaattcg gggctagagt atctggtgaa ccgtgcataa acgacctgtg     360
 54 attggactct ttttccttgc aaaatgtttt ccagcgg atg ttg agt ttt gcg acc     415
 55                                           Met Leu Ser Phe Ala Thr
 56                                            1               5
 58 ctt cgt ggc cgc att tca aca gtt gac gct gca aaa gcc gca cct ccg     463
 59 Leu Arg Gly Arg Ile Ser Thr Val Asp Ala Ala Lys Ala Ala Pro Pro
 60             10              15              20
 64 cca tcg cca cta gcc ccg att gat ctc act gac cat agt caa gtg gcc     511
 65 Pro Ser Pro Leu Ala Pro Ile Asp Leu Thr Asp His Ser Gln Val Ala
 66         25              30              35
 68 ggt gtg atg aat ttg gct gcg aga att ggc gat att ttg ctt tct tca     559
 69 Gly Val Met Asn Leu Ala Ala Arg Ile Gly Asp Ile Leu Leu Ser Ser
 70     40              45              50
 72 ggt acg tca aac agt gat acc aag gtg caa gtt cga gcg gtg acc tct     607
 73 Gly Thr Ser Asn Ser Asp Thr Lys Val Gln Val Arg Ala Val Thr Ser
 74 55              60              65              70
 76 gcg tat ggc ctg tac tat acg cat gtg gat atc acg ttg aat acg atc     655
 77 Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp Ile Thr Leu Asn Thr Ile
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78              75                80                85
80 acc atc ttc acc aac atc ggt gtg gag agg aag atg ccg gtc aac gtg      703
81 Thr Ile Phe Thr Asn Ile Gly Val Glu Arg Lys Met Pro Val Asn Val
82              90                95                100
84 ttt cat gtt gtg ggc aag ttg gac acc aac ttc tcc aaa ctg tct gag      751
85 Phe His Val Val Gly Lys Leu Asp Thr Asn Phe Ser Lys Leu Ser Glu
86         105               110               115
88 gtt gac cgt ttg atc cgt tcc att cag gct ggt gct acc ccg cct gag      799
89 Val Asp Arg Leu Ile Arg Ser Ile Gln Ala Gly Ala Thr Pro Pro Glu
90      120               125               130
92 gtt gcc gag aaa att ctg gac gag ttg gag caa tcg cct gcg tct tat      847
93 Val Ala Glu Lys Ile Leu Asp Glu Leu Glu Gln Ser Pro Ala Ser Tyr
94 135               140               145               150
96 ggt ttc cct gtt gcg ttg ctt ggc tgg gca atg atg ggt ggc gct gtt      895
97 Gly Phe Pro Val Ala Leu Leu Gly Trp Ala Met Met Gly Gly Ala Val
98              155               160               165
100 gct gtg ctg ttg ggt ggt gga tgg cag gtt tcc cta att gct ttt att     943
101 Ala Val Leu Leu Gly Gly Gly Trp Gln Val Ser Leu Ile Ala Phe Ile
102             170               175               180
104 acc gcg ttc acg atc att gcc acg acg tca ttt ttg gga aag aag ggt     991
105 Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser Phe Leu Gly Lys Lys Gly
106             185               190               195
108 ttg cct act ttc ttc caa aat gtt gtt ggt ggt ttt att gcc acg ctg     1039
109 Leu Pro Thr Phe Phe Gln Asn Val Val Gly Gly Phe Ile Ala Thr Leu
110     200               205               210
112 cct gca tcg att gct tat tct ttg gcg ttg caa ttt ggt ctt gag atc     1087
113 Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu Gln Phe Gly Leu Glu Ile
114 215               220               225               230
116 aaa ccg agc cag atc atc gca tct gga att gtt gtg ctg ttg gca ggt     1135
117 Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile Val Val Leu Leu Ala Gly
118             235               240               245
120 ttg aca ctt gtg caa tct ctg cag gac ggc atc acg ggc gct ccg gtg     1183
121 Leu Thr Leu Val Gln Ser Leu Gln Asp Gly Ile Thr Gly Ala Pro Val
122             250               255               260
124 aca gca agt gca cga ttt ttt gaa aca ctc ctg ttt acc ggc ggc att     1231
125 Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu Leu Phe Thr Gly Gly Ile
126             265               270               275
128 gtt gct ggc gtg ggt ttg ggc att cag ctt tct gaa atc ttg cat gtc     1279
129 Val Ala Gly Val Gly Leu Gly Ile Gln Leu Ser Glu Ile Leu His Val
130     280               285               290
132 atg ttg cct gcc atg gag tcc gct gca gca cct aat tat tcg tct aca     1327
133 Met Leu Pro Ala Met Glu Ser Ala Ala Ala Pro Asn Tyr Ser Ser Thr
134 295               300               305               310
136 ttc gcc cgc att atc gct ggt ggc gtc acc gca gcg gcc ttc gca gtg     1375
137 Phe Ala Arg Ile Ile Ala Gly Gly Val Thr Ala Ala Ala Phe Ala Val
138             315               320               325
140 ggt tgt tac gcg gag tgg tcc tcg gtg att att gcg ggg ctt act gcg     1423
141 Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile Ile Ala Gly Leu Thr Ala
142             330               335               340
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144 ctg atg ggt tct gcg ttt tat tac ctc ttc gtt gtt tat tta ggc ccc    1471
145 Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe Val Val Tyr Leu Gly Pro
146         345                 350                 355
148 gtc tct gcc gct gcg att gct gca aca gca gtt ggt ttc act ggt ggt    1519
149 Val Ser Ala Ala Ala Ile Ala Ala Thr Ala Val Gly Phe Thr Gly Gly
150         360                 365                 370
152 ttg ctt gcc cgt cga ttc ttg att cca ccg ttg att gtg gcg att gcc    1567
153 Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro Leu Ile Val Ala Ile Ala
154 375                 380                 385                 390
156 ggc atc aca cca atg ctt cca ggt cta gca att tac cgc gga atg tac    1615
157 Gly Ile Thr Pro Met Leu Pro Gly Leu Ala Ile Tyr Arg Gly Met Tyr
158                 395                 400                 405
160 gcc acc ttg aat gat caa aca ctc atg ggt ttc acc aac att gcg gtt    1663
161 Ala Thr Leu Asn Asp Gln Thr Leu Met Gly Phe Thr Asn Ile Ala Val
162             410                 415                 420
164 gct tta gcc act gct tca tca ctt gcc gct ggc gtg gtt ttg ggt gag    1711
165 Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala Gly Val Val Leu Gly Glu
166         425                 430                 435
168 tgg att gcc cgc agg cta cgt cgt cca cca cgc ttc aac cca tac cgt    1759
169 Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro Arg Phe Asn Pro Tyr Arg
170     440                 445                 450
172 gca ttt acc aag gcg aat gag ttc tcc ttc cag gag gaa gct gag cag    1807
173 Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe Gln Glu Glu Ala Glu Gln
174 455                 460                 465                 470
176 aat cag cgc cgg cag aga aaa cgt cca aag act aat caa aga ttc ggt    1855
177 Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys Thr Asn Gln Arg Phe Gly
178                 475                 480                 485
180 aat aaa agg taaaaatcaa cctgcttagg cgtctttcgc ttaaatagcg           1904
181 Asn Lys Arg
184 tagaatatcg ggtcgatcgc ttttaaacac tcaggaggat ccttgccggc caaaatcacg    1964
186 gacactcgtc ccaccccaga atcccttcac gctgttgaag aggaaaccgc agccggtgcc    2024
188 cgcaggattg ttgccaccta ttctaaggac ttcttcgacg gcgtcacttt gatgtgcatg    2084
190 ctcggcgttg aacctcaggg cctgcgttac accaaggtcg cttctgaaca cgaggaagct    2144
192 cagccaaaga aggctacaaa gcggactcgt aaggcaccag ctaagaaggc tgctgctaag    2204
194 aaaacgacca agaagaccac taagaaaact actaaaaaga ccaccgcaaa gaagaccaca    2264
196 aagaagtctt aagccggatc ttatatggat gattccaata gctttgtagt tgttgctaac    2324
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204 caccctgttg tcctcactgc aagtgactat gaaggcttct acgagggctt ttcaaacgca    2564
206 acgctgtggc ctctttttcca cgatttgatt gttactccgg tgtacaacac cgattggtgg    2624
208 catgcgtttc gggaagtaaa cctcaagttc gctgaagccg tgagccaagt ggcggcacac    2684
210 ggtgccactg tgtgggtgca ggactatcag ctgttgctgg ttcctggcat tttgcgccag    2744
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214 ttccgtcagc tgc                                                       2817
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222 <212> TYPE: PRT
224 <213> ORGANISM: Corynebacterium glutamicum ATCC14752
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234             20                  25                  30
237 Asp His Ser Gln Val Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly
238         35                  40                  45
241 Asp Ile Leu Leu Ser Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln
242     50                  55                  60
245 Val Arg Ala Val Thr Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp
246 65                  70                  75                  80
249 Ile Thr Leu Asn Thr Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg
250                 85                  90                  95
253 Lys Met Pro Val Asn Val Phe His Val Val Gly Lys Leu Asp Thr Asn
254             100                 105                 110
257 Phe Ser Lys Leu Ser Glu Val Asp Arg Leu Ile Arg Ser Ile Gln Ala
258             115                 120                 125
261 Gly Ala Thr Pro Pro Glu Val Ala Glu Lys Ile Leu Asp Glu Leu Glu
262     130                 135                 140
265 Gln Ser Pro Ala Ser Tyr Gly Phe Pro Val Ala Leu Leu Gly Trp Ala
266 145             150                 155                 160
269 Met Met Gly Gly Ala Val Ala Val Leu Leu Gly Gly Gly Trp Gln Val
270             165                 170                 175
273 Ser Leu Ile Ala Phe Ile Thr Ala Phe Thr Ile Ile Ala Thr Thr Ser
274             180                 185                 190
277 Phe Leu Gly Lys Lys Gly Leu Pro Thr Phe Phe Gln Asn Val Val Gly
278         195                 200                 205
281 Gly Phe Ile Ala Thr Leu Pro Ala Ser Ile Ala Tyr Ser Leu Ala Leu
282     210                 215                 220
285 Gln Phe Gly Leu Glu Ile Lys Pro Ser Gln Ile Ile Ala Ser Gly Ile
286 225             230                 235                 240
289 Val Val Leu Leu Ala Gly Leu Thr Leu Val Gln Ser Leu Gln Asp Gly
290             245                 250                 255
293 Ile Thr Gly Ala Pro Val Thr Ala Ser Ala Arg Phe Phe Glu Thr Leu
294             260                 265                 270
297 Leu Phe Thr Gly Gly Ile Val Ala Gly Val Gly Leu Gly Ile Gln Leu
298         275                 280                 285
301 Ser Glu Ile Leu His Val Met Leu Pro Ala Met Glu Ser Ala Ala Ala
302     290                 295                 300
305 Pro Asn Tyr Ser Ser Thr Phe Ala Arg Ile Ile Ala Gly Gly Val Thr
306 305             310                 315                 320
309 Ala Ala Ala Phe Ala Val Gly Cys Tyr Ala Glu Trp Ser Ser Val Ile
310             325                 330                 335
313 Ile Ala Gly Leu Thr Ala Leu Met Gly Ser Ala Phe Tyr Tyr Leu Phe
314         340                 345                 350
317 Val Val Tyr Leu Gly Pro Val Ser Ala Ala Ala Ile Ala Ala Thr Ala
318         355                 360                 365
321 Val Gly Phe Thr Gly Gly Leu Leu Ala Arg Arg Phe Leu Ile Pro Pro
322     370                 375                 380
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325 Leu Ile Val Ala Ile Ala Gly Ile Thr Pro Met Leu Pro Gly Leu Ala
326 385                 390                 395                 400
329 Ile Tyr Arg Gly Met Tyr Ala Thr Leu Asn Asp Gln Thr Leu Met Gly
330                 405                 410                 415
333 Phe Thr Asn Ile Ala Val Ala Leu Ala Thr Ala Ser Ser Leu Ala Ala
334                 420                 425                 430
337 Gly Val Val Leu Gly Glu Trp Ile Ala Arg Arg Leu Arg Arg Pro Pro
338             435                 440                 445
341 Arg Phe Asn Pro Tyr Arg Ala Phe Thr Lys Ala Asn Glu Phe Ser Phe
342     450                 455                 460
345 Gln Glu Glu Ala Glu Gln Asn Gln Arg Arg Gln Arg Lys Arg Pro Lys
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349 Thr Asn Gln Arg Phe Gly Asn Lys Arg
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360 <213> ORGANISM: Corynebacterium glutamicum ATCC13032
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364 <221> NAME/KEY: CDS
366 <222> LOCATION: (280)..(1746)
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374 cgccactcca gcaccgcaga tgctgatgat caacaactac gaatacgtat cttagcgtat       180
376 gtgtacatca caatggaatt cggggctaga gtatctggtg aaccgtgcat aaacgacctg       240
378 tgattggact ctttttcctt gcaaaatgtt ttccagcgg atg ttg agt ttt gcg        294
379                                               Met Leu Ser Phe Ala
380                                               1               5
383 acc ctt cgt ggc cgc att tca aca gtt gac gct gca aaa gcc gca cct       342
384 Thr Leu Arg Gly Arg Ile Ser Thr Val Asp Ala Ala Lys Ala Ala Pro
385                 10                  15                  20
387 ccg cca tcg cca cta gcc ccg att gat ctc act gac cat agt caa gtg       390
388 Pro Pro Ser Pro Leu Ala Pro Ile Asp Leu Thr Asp His Ser Gln Val
389             25                  30                  35
391 gcc ggt gtg atg aat ttg gct gcg aga att ggc gat att ttg ctt tct       438
392 Ala Gly Val Met Asn Leu Ala Ala Arg Ile Gly Asp Ile Leu Leu Ser
393             40                  45                  50
395 tca ggt acg tca aat agt gac acc aag gta caa gtt cga gca gtg acc       486
396 Ser Gly Thr Ser Asn Ser Asp Thr Lys Val Gln Val Arg Ala Val Thr
397     55                  60                  65
399 tct gcg tac ggt ttg tac tac acg cac gtg gat atc acg ttg aat acg       534
400 Ser Ala Tyr Gly Leu Tyr Tyr Thr His Val Asp Ile Thr Leu Asn Thr
401 70                  75                  80                  85
403 atc acc atc ttc acc aac atc ggt gtg gag agg aag atg ccg gtc aac       582
404 Ile Thr Ile Phe Thr Asn Ile Gly Val Glu Arg Lys Met Pro Val Asn
405                 90                  95                  100
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408 Val Phe His Val Val Gly Lys Leu Asp Thr Asn Phe Ser Lys Leu Ser
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VERIFICATION SUMMARY
DATE: 12/18/2002
PATENT APPLICATION: **US/09/783,338B**
TIME: 12:10:22

Input Set : **A:\ziegler.ST25.txt**
Output Set: **N:\CRF4\12182002\I783338B.raw**

L:20 M:270 C: Current Application Number differs, Replaced Current Application No
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date